Amendments to the claims:
This listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1-31 (canceled)

Claim 32 (previously presented): A method for identifying single nucleotide polymorphic sites in a genome of a species of interest, comprising:

(a) isolating a plurality of DNA fragments from the genome of a population of individual representatives of the species of interest, wherein each fragment corresponds to a location of the genome and the fragments are between about 0.1 kb and 10.0 kb;

(b) sequencing the DNA fragments to determine the nucleotide sequences of each fragment, and

(c) comparing the sequence of each fragment to corresponding fragments that correspond to the same location of the genome from other individual representatives of the species of interest to identify single nucleotide polymorphic sites, wherein each single nucleotide polymorphic site comprises a single nucleotide polymorphism, and each single nucleotide polymorphic site is immediately flanked by a 3' and 5' invariant nucleotide sequence and the species of interest is a mammal and the comparison is made among mammals of the same species.

Claim 33 (previously presented): A method according to claim 32, wherein the plurality of DNA fragments is from a population of between 10 to 100 individual representatives of the same species.

Claim 34 (previously presented): A method according to claim 32, wherein the plurality of DNA fragments is from a population of between 100 to 1000 individual representatives of the same species.

Claim 35 (previously presented): A method according to claim 32, wherein the plurality of DNA fragments is from a population of between 100 and 10,000 individual representatives of the same species.

Claim 36 (previously presented): A method according to claim 32, wherein the fragments are between 0.5 kb and 3.0 kb.

Claim 37 (previously presented): A method according to claim 32, wherein the fragments are sequenced by dideoxy sequencing.

Claim 38 (previously presented): A method according to claim 32, wherein the fragments are isolated by amplification using oligonucleotide primers.

Claim 39 (previously presented): A method for determining allelic frequency at a single nucleotide polymorphic site, comprising:

(a) isolating a plurality of DNA fragments from a population of two or more individual representatives of a species of interest, wherein each fragment corresponds to a location of the genome and the fragments are between about 0.1 kb and 10.0 kb;

(b) sequencing the DNA fragments to determine the nucleotide sequences of each fragment;

(c) comparing the sequence of each fragment to corresponding DNA fragments from different individual representatives of the species of interest and identifying single nucleotide polymorphic sites having at least two alleles, wherein each single nucleotide polymorphic site comprises a single nucleotide polymorphism, and each single nucleotide polymorphic site is immediately flanked by a 3' and 5' invariant nucleotide sequence and the species of interest is a mammal of the same species and the comparison is made among mammals of the same species,

(d) determining the base identity of each allele present in the location of the genome, and

(e) calculating the allelic frequency for each allele by dividing the frequency at which each allele appears in the sample set by the total number of individuals.

Claim 40 (previously presented): A method according to claim 39, wherein the plurality of DNA fragments is from a population of between 10 to 100 individual representatives of the same species.

Claim 41 (previously presented): A method according to claim 39, wherein the plurality of DNA fragments is from a population of between 100 to 1000 individual representatives of the same species.

Claim 42 (previously presented): A method according to claim 39, wherein the plurality of DNA fragments is from a population of between 100 and 10,000 individual representatives of the same species.

Claim 43 (previously presented): A method according to claim 39, wherein the fragments are between 0.5 kb and 3.0 kb.

Claim 44 (previously presented): A method according to claim 39, wherein the fragments are sequenced by dideoxy sequencing.

Claim 45 (previously presented): A method according to claim 39, wherein the fragments are isolated by amplification using oligonucleotide primers.

Claim 46 (previously presented): A method according to claim 32, wherein the method is used to identify a mammal.

Claim 47 (previously presented): A method according to claim 32, wherein the method is used to determine parentage of the mammal.

Claim 48 (previously presented): A method according to claim 32, wherein the mammal is selected from the group consisting of human, non-human primates, dogs, cats, cattle, sheep and horses.

Claim 49 (previously presented): A method according to claim 47, wherein the mammal is a horse.

Claim 50 (previously presented): A method according to claim 46, wherein the mammal is a horse.

Claim 51 (previously presented): A method according to claim 32, wherein the mammal is a human.

Claim 52 (previously presented): A method according to claim 32, wherein the mammal is a horse.

Claim 53 (previously presented): A method according to claim 39, wherein the mammal is selected from the group consisting of human, non-human primates, dogs, cats, cattle, sheep and horses.

Claim 54 (previously presented): A method according to claim 39, wherein the mammal is a human.

Claim 55 (previously presented): A method according to claim 39, wherein the mammal is a horse.

Claim 56 (previously presented): A method of determining the likelihood that a horse is or is not an offspring of a putative parent of the same breed, comprising:

a) isolating a plurality of DNA fragments from upper and lower strands of putative offspring horse genomic DNA, the upper and lower strands comprising single nucleotide polymorphic sites that each have an allelic frequency of at least 0.20;

b) isolating a plurality of DNA fragments from upper and lower strands of putative parental horse genomic DNA, the upper and lower strands comprising single nucleotide polymorphic sites that each have an allelic frequency of at least 0.20,

c) identifying the single nucleotide polymorphic sites of the putative parental genomic DNA and the putative offspring genomic DNA by determining the nucleotide base identity at each single nucleotide polymorphic site, wherein each single nucleotide polymorphic site comprises a single nucleotide polymorphism, and each single nucleotide polymorphic site is immediately flanked by a 3' and 5' invariant nucleotide sequence; and

d) comparing single nucleotide polymorphic sites that match between the putative parental genomic DNA and the putative offspring genomic DNA, thereby determining the likelihood that the horse is or is not the offspring of the putative parent.

Claim 57 (previously presented): A method according to claim 56, wherein the putative parent or offspring is a male.

Claim 58 (previously presented): A method according to claim 56, wherein the putative parent or offspring is a female.

Claim 59 (currently amended): A method of determining the likelihood that a mammal is or is not an offspring of a putative parent mammal of the same species, comprising:

a) isolating a plurality of DNA fragments from upper and lower strands of putative offspring mammalian genomic DNA, the upper and lower strands comprising known single nucleotide polymorphic sites that each have an allelic frequency of at least 0.20;

b) isolating a plurality of DNA fragments from upper and lower strands of putative parental mammalian genomic DNA, the upper and lower strands comprising known single nucleotide polymorphic sites that each have an allelic frequency of at least 0.20;

c) identifying the single nucleotide polymorphic sites of the putative parental genomic DNA and the putative offspring genomic DNA by determining the nucleotide base identity at each known single nucleotide polymorphic site using a set of probes, each probe having the same nucleotide sequence, wherein each single nucleotide polymorphic site comprises a single nucleotide polymorphism, and each single nucleotide polymorphic site is immediately flanked by a 3' and 5' invariant nucleotide sequence; and

d) comparing only known single nucleotide polymorphic sites that match between the putative parental genomic DNA and the putative offspring genomic DNA, thereby determining the likelihood that the mammal is or is not the offspring of the putative parent mammal.

Claim 60 (currently amended): A method of determining the likelihood that a mammal is or is not an offspring of a putative parent mammal of the same species, comprising:

a) isolating a plurality of DNA fragments from upper and lower strands of putative offspring mammalian genomic DNA, the upper and lower strands comprising known single nucleotide polymorphic sites that each have an allelic frequency of at least 0.20;

b) isolating a plurality of DNA fragments from upper and lower strands of putative parental mammalian genomic DNA, the upper and lower strands comprising known single nucleotide polymorphic sites that each have an allelic frequency of at least 0.20;

c) identifying the single nucleotide polymorphic sites of the putative parental genomic DNA and the putative offspring genomic DNA by determining the nucleotide base identity at each known single nucleotide polymorphic site, wherein each single nucleotide polymorphic site comprises a single nucleotide polymorphism, and each single nucleotide polymorphic site is immediately flanked by a 3' and 5' invariant nucleotide sequence; and

d) comparing known single nucleotide polymorphic sites that match between the putative parental genomic DNA and the putative offspring genomic DNA, thereby determining the likelihood that the mammal is or is not the offspring of the putative parent ~~according to claim 59~~, wherein the mammal is a horse and the known polymorphic sites and 3' and 5' invariant nucleotide sequences ~~comprises~~ comprise at least one of SEQ ID NOs: 1-72.

Claim 61 (previously presented): A method of determining the likelihood that a mammal is or is not an offspring of a putative parent mammal of the same species, comprising:

a) isolating a plurality of DNA fragments from upper and lower strands of putative offspring mammalian genomic DNA, the upper and lower strands comprising known single nucleotide polymorphic sites that each have an allelic frequency of at least 0.20;

b) isolating a plurality of DNA fragments from upper and lower strands of putative parental mammalian genomic DNA, the upper and lower strands comprising known single nucleotide polymorphic sites that each have an allelic frequency of at least 0.20;

c) identifying the single nucleotide polymorphic sites of the putative parental genomic DNA and the putative offspring genomic DNA by separately determining the nucleotide base identity at each known single nucleotide polymorphic site, wherein each single nucleotide polymorphic site comprises a single nucleotide polymorphism, and each single nucleotide polymorphic site is immediately flanked by a 3' and 5' invariant nucleotide sequence; and

d) comparing eighteen known single nucleotide polymorphic sites that match between the putative parental genomic DNA and the putative offspring genomic DNA, thereby determining the likelihood that the mammal is or is not the offspring of the putative parent mammal.